

Amendments to the Specification

Please replace the paragraph at page 21, lines 3-27 with the following amended paragraph:

TN9 was chosen for further analysis based on its high affinity for tenascin-C. We first searched for a minimal sequence necessary for high affinity binding. Using standard techniques (Green et al, *supra*), it was discovered that nucleotides 3' of nucleotide 55 were required for binding to tenascin-C, while no nucleotides could be removed from the 5' end without loss of affinity. To further decrease the TN9's length from 55 nucleotides and retain high affinity binding, we then attempted to define internal deletions of TN9. The first 55 nucleotides of TN9, along with the first 55 nucleotides of related family II ligands TN7, TN21, and TN41, were input into a computer algorithm to determine possible RNA secondary structure foldings (mfold 3.0, ~~accessed at~~ <http://www.ibc.wustl.edu/~zucker/>. M. Zuker, D.H. Mathews & D.H. Turner. Algorithms and Thermodynamics for RNA Secondary Structure Prediction: A Practical Guide. In: RNA Biochemistry and Biotechnology, J. Barciszewski & B.F.C. Clark, eds., NATO ASI Series, Kluwer Academic Publishers, (1999)). Among many potential RNA foldings predicted by the algorithm, a structure common to each oligonucleotide was found. This structure, represented by oligonucleotide TTA1 in **Figure 2**, contains three stems that meet at a single junction, a so-called 3-stem junction. This folding places the most highly conserved nucleotides of family II oligonucleotides at the junction area. In comparing TN9, TN7, TN21, and TN41, the second stem was of variable length and sequence, suggesting that extension of the second stem is not required for binding to tenascin-C. Testing this hypothesis on TN9, we found that nucleotides 10-26 could be replaced with an ethylene glycol linker, (CH₂CH₂O)₆. The linker serves as a substitute loop and decreases the size of the aptamer. Additionally, four-nucleotide loops (CACU or GAGA) that replace nucleotides 10-26 produce sequences with high affinity for tenascin-C. It would be well within one skilled in the art to determine other nucleotide loops or other spacers that could replace nucleotides 10-26 to produce sequences with high affinity for tenascin-C.